SEQ ID NO.1

FIG.1 a

```
GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC      59 (UPPER: SEQ ID NO:
                                                                  19 (LOWER: SEQ ID NO:4

TTCCCTTCACTACAAAACTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT     119
                                                                  39

CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC     179
                                                                  59

TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTTATGCACAGGGTGGAACAAG     239
                                                                  79

ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC     299
 M  D  Y  Q  V  S  S  P  I  Y  D  I  N  Y  Y  T  S  E  P  C      99

CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG     359
 Q  K  I  N  V  K  Q  I  A  A  R  L  L  P  P  L  Y  S  L  V     119

TTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG     419
 F  I  F  G  F  V  G  N  M  L  V  I  L  I  L  I  N  C  K  R     139

CTCAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT     479
 L  K  S  M  T  D  I  Y  L  L  N  L  A  I  S  D  L  F  F  L     159

CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGACTTTGGAAATACAATG     539
 L  T  V  P  F  W  A  H  Y  A  A  A  Q  W  D  F  G  N  T  M     179

TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC     599
 C  Q  L  L  T  G  L  Y  F  I  G  F  F  S  G  I  F  F  I  I     199

CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAAGCCAGG     659
 L  L  T  I  D  R  Y  L  A  V  V  H  A  V  F  A  L  K  A  R     219

ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGCGTCT     719
 T  V  T  F  G  V  V  T  S  V  I  T  W  V  V  A  V  F  A  S     239

CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT     779
 L  P  G  I  I  F  T  R  S  Q  K  E  G  L  H  Y  T  C  S  S     259

CATTTTCCATACA
 H  F  P  Y
```

```
GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC      59 (UPPER: SEQ ID NO:2,
                                                                  19 (LOWER: SEQ ID NO.5,

TTCCCTTCACTACAAAACTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT     119
                                                                  39

CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC     179
                                                                  59

TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTTATTTATGCACAGGGTGGAACAAG    239
                                                                  79

ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC     299
 M  D  Y  Q  V  S  S  P  I  Y  D  I  N  Y  Y  T  S  E  P  C      99

CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG    359
 Q  K  I  N  V  K  Q  I  A  A  R  L  L  P  P  L  Y  S  L  V     119

TTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG    419
 F  I  F  G  F  V  G  N  M  L  V  I  L  I  L  I  N  C  K  R     139

CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT    479
 L  K  S  M  T  D  I  Y  L  L  N  L  A  I  S  D  L  F  F  L     159

CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGACTTTGGAAATACAATG    539
 T  V  P  F  W  A  H  Y  A  A  A  Q  W  D  F  G  N  T  M      179

TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC    599
 C  Q  L  L  T  G  L  Y  F  I  G  F  F  S  G  I  F  F  I  I     199

CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAAGCCAGG    659
 L  L  T  I  D  R  Y  L  A  V  V  H  A  V  F  A  L  K  A  R     219

ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGCGTCT    719
 T  V  T  F  G  V  V  T  S  V  I  T  W  V  V  A  V  F  A  S     239

CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT    779
 L  P  G  I  I  F  T  R  S  Q  K  E  G  L  H  Y  T  C  S  S     259

CATTTTCCATACAGTCAGTATCAATTCTGGAAGAATTTCCAGACATTAAAGATAGTCATC    839
 H  F  P  Y  S  Q  Y  Q  F  W  K  N  F  Q  T  L  K  I  V  I     279
```

SEQ ID NO.2 FIG.1b

```
TTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCGGGAATCCTAAAAACT    899
 L  G  L  V  L  P  L  L  V  M  V  I  C  Y  S  G  I  L  K  T     299

CTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGGGCTGTGAGGCTTATCTTCACCATC    959
 L  L  R  C  R  N  E  K  K  R  H  R  A  V  R  L  I  F  T  I     319

ATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACATTGTCCTTCTCCTGAACACCTTC   1019
 M  I  V  Y  F  L  F  W  A  P  Y  N  I  V  L  L  L  N  T  F     339

CAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTAACAGGTTGGACCAAGCTATGCAG   1079
 Q  E  F  F  G  L  N  N  C  S  S  S  N  R  L  D  Q  A  M  Q     359

GTGACAGAGACTCTTGGGATGACGCACTGCTGCATCAACCCCATCATCTATGCCTTTGTC   1139
 V  T  E  T  L  G  M  T  H  C  C  I  N  P  I  I  Y  A  F  V     379

GGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTTCCAAAAGCACATTGCCAAACGCTTC   1199
 G  E  K  F  R  N  Y  L  L  V  F  F  Q  K  H  I  A  K  R  F     399

TGCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCGAGCGAGCAAGCTCAGTTTACACC   1259
 C  K  C  C  S  I  F  Q  Q  E  A  P  E  R  A  S  S  V  Y  T     419

CGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTGTGACACGGACTCAAGTGGGCTGGT   1319
 R  S  T  G  E  Q  E  I  S  V  G  L  *                          439

GACCCAGTCAGAGTTGTGCACATGGCTTAGTTTTCATACACAGCCTGGGCTGGGGGTNGG   1379
                                                                459

TTGGNNGAGGTCTTTTTTAAAAGGAAGTTACTGTTATAGAGGGTCTAAGATTCATCCATT   1439
                                                                479

TATTTGGCATCTGTTTAAAGTAGATTAGATCCGAATTC
```

SEQ ID NO.2 (SUITE)

FIG.1c

```
GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC      59 (UPPER: SEQ ID NO.3
                                                                  19 LOWER: SEQ ID NO.4

TTCCCTTCACTACAAAACTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT     119
                                                                  39

CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC     179
                                                                  59

TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTTATGCACAGGGTGGAACAAG     239
                                                                  79

ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC     299
 M  D  Y  Q  V  S  S  P  I  Y  D  I  N  Y  Y  T  S  E  P  C      99

CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG     359
 Q  K  I  N  V  K  Q  I  A  A  R  L  L  P  P  L  Y  S  L  V     119

TTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG     419
 F  I  F  G  F  V  G  N  M  L  V  I  L  I  L  I  N  C  K  R     139

CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT     479
 L  K  S  M  T  D  I  Y  L  L  N  L  A  I  S  D  L  F  F  L     159

CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGACTTTGGAAATACAATG     539
 L  T  V  P  F  W  A  H  Y  A  A  A  Q  W  D  F  G  N  T  M     179

TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC     599
 C  Q  L  L  T  G  L  Y  F  I  G  F  F  S  G  I  F  F  I  I     199

CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAAGCCAGG     659
 L  L  T  I  D  R  Y  L  A  V  V  H  A  V  F  A  L  K  A  R     219

ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGCGTCT     719
 T  V  T  F  G  V  V  T  S  V  I  T  W  V  V  A  V  F  A  S     239

CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT     779
 L  P  G  I  I  F  T  R  S  Q  K  E  G  L  H  Y  T  C  S  S     259

CATTTTCCATACATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGT     839
 H  F  P  Y  I  K  D  S  H  L  G  A  G  P  A  A  A  C  H  G     279
```

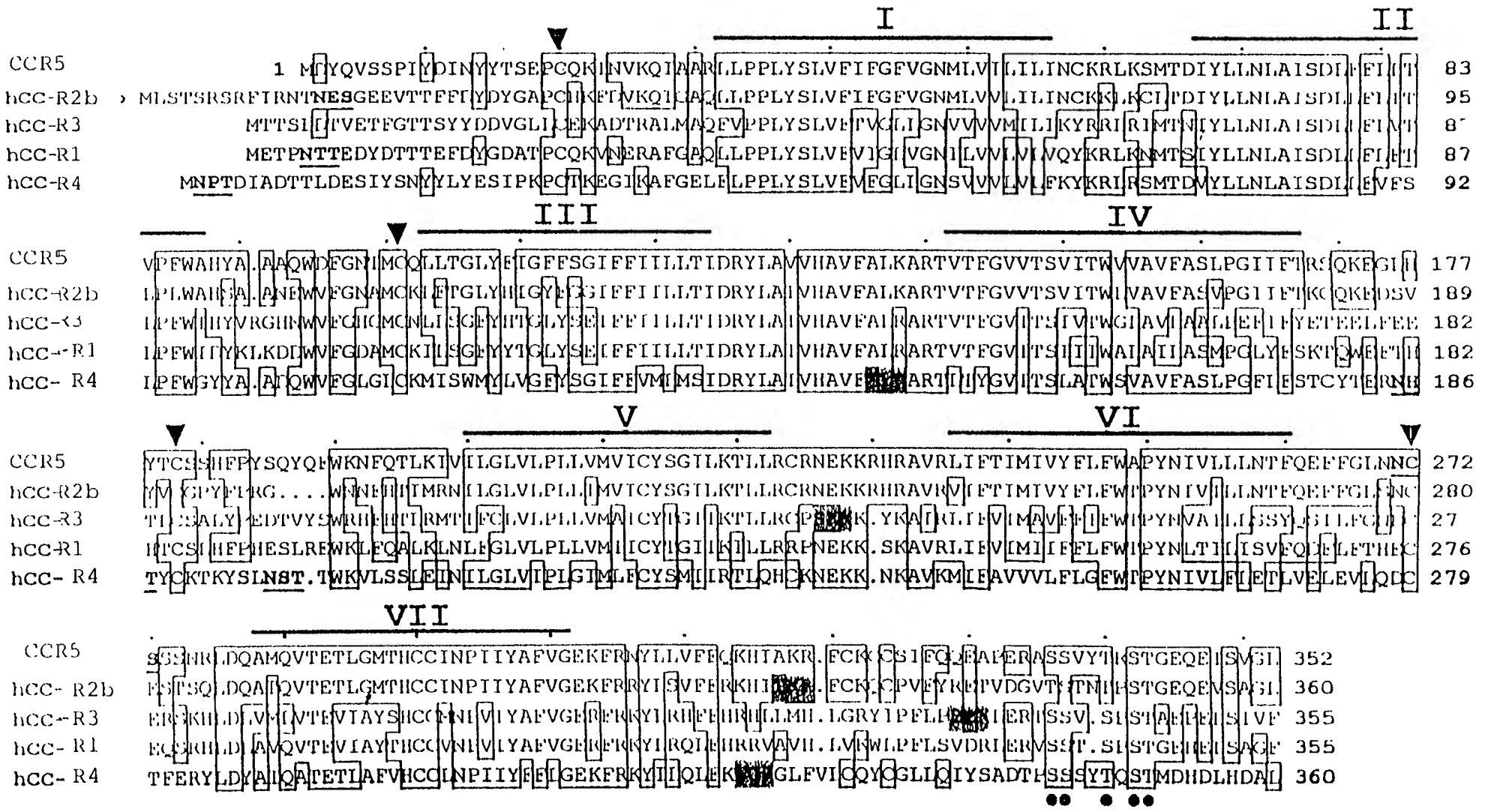
SEQ ID NO.3 FIG.1d

```
CATCTGCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCA    899
 H  L  L  L  G  N  P  K  N  S  A  S  V  S  K  *                 299

CAGGGCTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTA    959
                                                                319

CAACATTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAG    1019
                                                                339

CTCTAACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTG    1079
                                                                359

CATCAACCCCATCATCTATGCCTTTGTCGGGGAGAAGTTCAGAAACTACCTCTTAGTCTT    1139
                                                                379

CTTCCAAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGC    1199
                                                                399

TCCCGAGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGG    1259
                                                                419

CTTGTGACACGGACTCAAGTGGGCTGGTGACCCAGTCAGAGTTGTGCACATGGCTTAGTT    1319
                                                                439

TTCATACACAGCCTGGGCTGGGGGTNGGTTGGNNGAGGTCTTTTTTTAAAAGGAAGTTACT    1379
                                                                459

GTTATAGAGGGTCTAAGATTCATCCATTTATTTGGCATCTGTTTAAAGTAGATTAGATCC    1439
                                                                479

GAATTC
```

SEQ ID NO.3 (SUITE)

FIG.1e

FIG.2



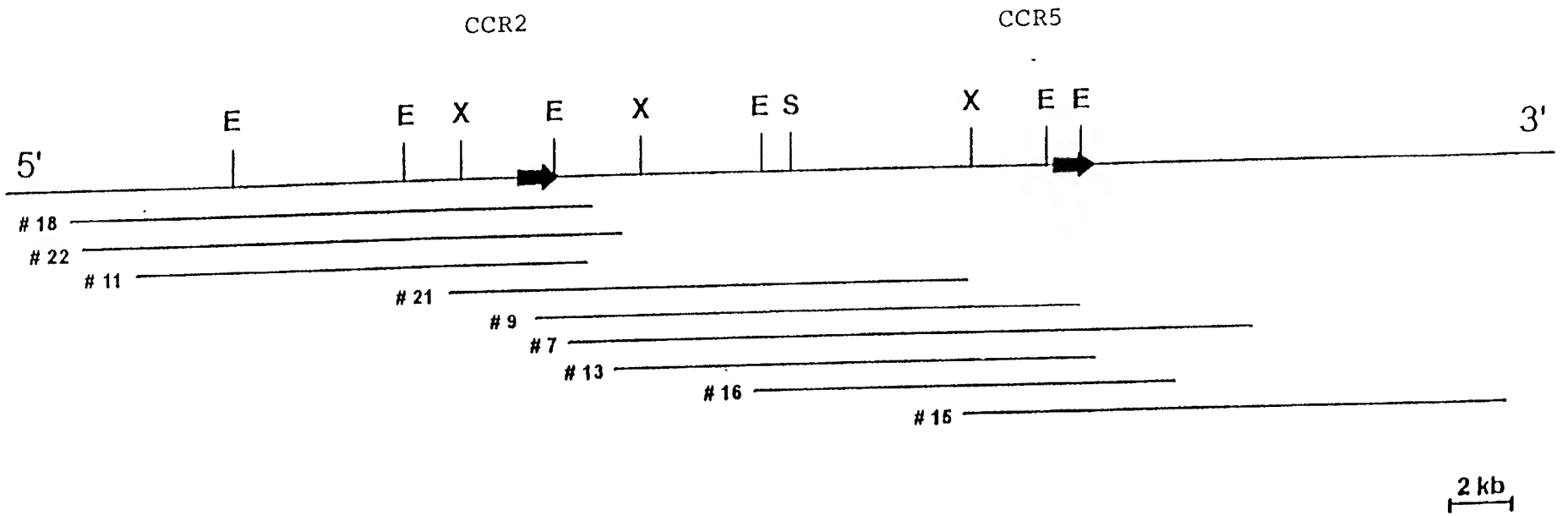


FIG. 3

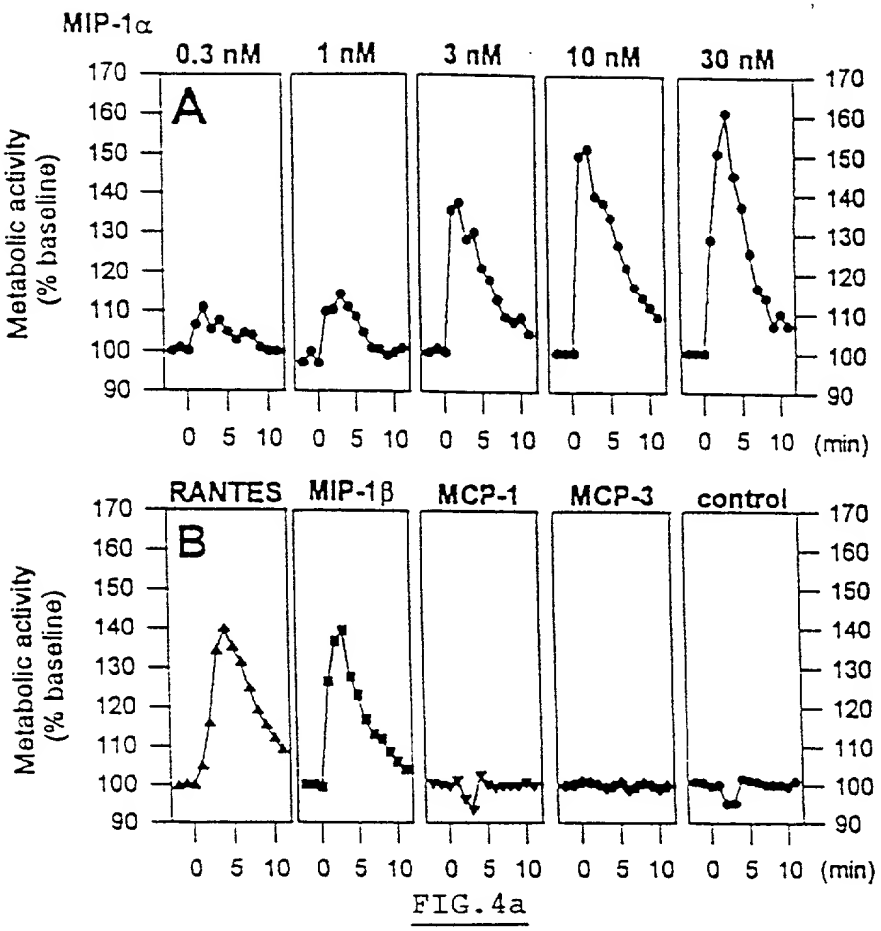

MIP-1α
0.3 nM
1 nM
3 nM
10 nM
30 nM
A
Metabolic activity
(% baseline)
170
160
150
140
130
120
110
100
90
0 5 10
(min)
RANTES
MIP-1β
MCP-1
MCP-3
control
B

FIG.4a

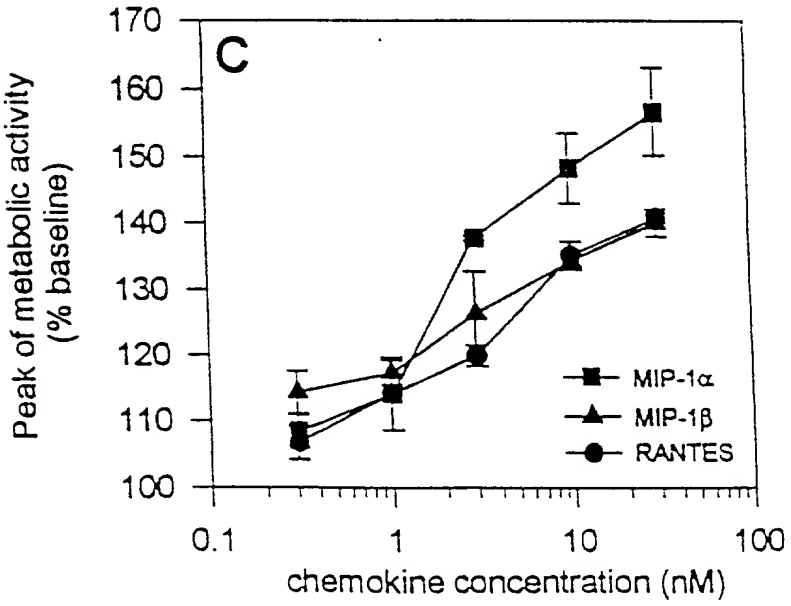

C
Peak of metabolic activity
(% baseline)
170
160
150
140
130
120
110
100
0.1
1
10
100
chemokine concentration (nM)
MIP-1α
MIP-1β
RANTES

FIG.4b

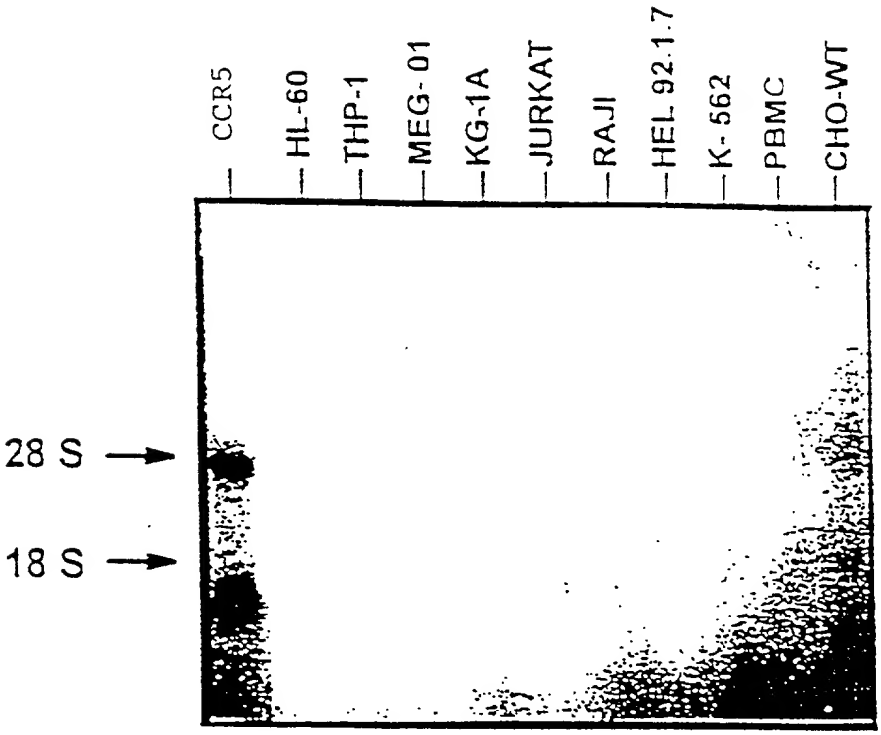
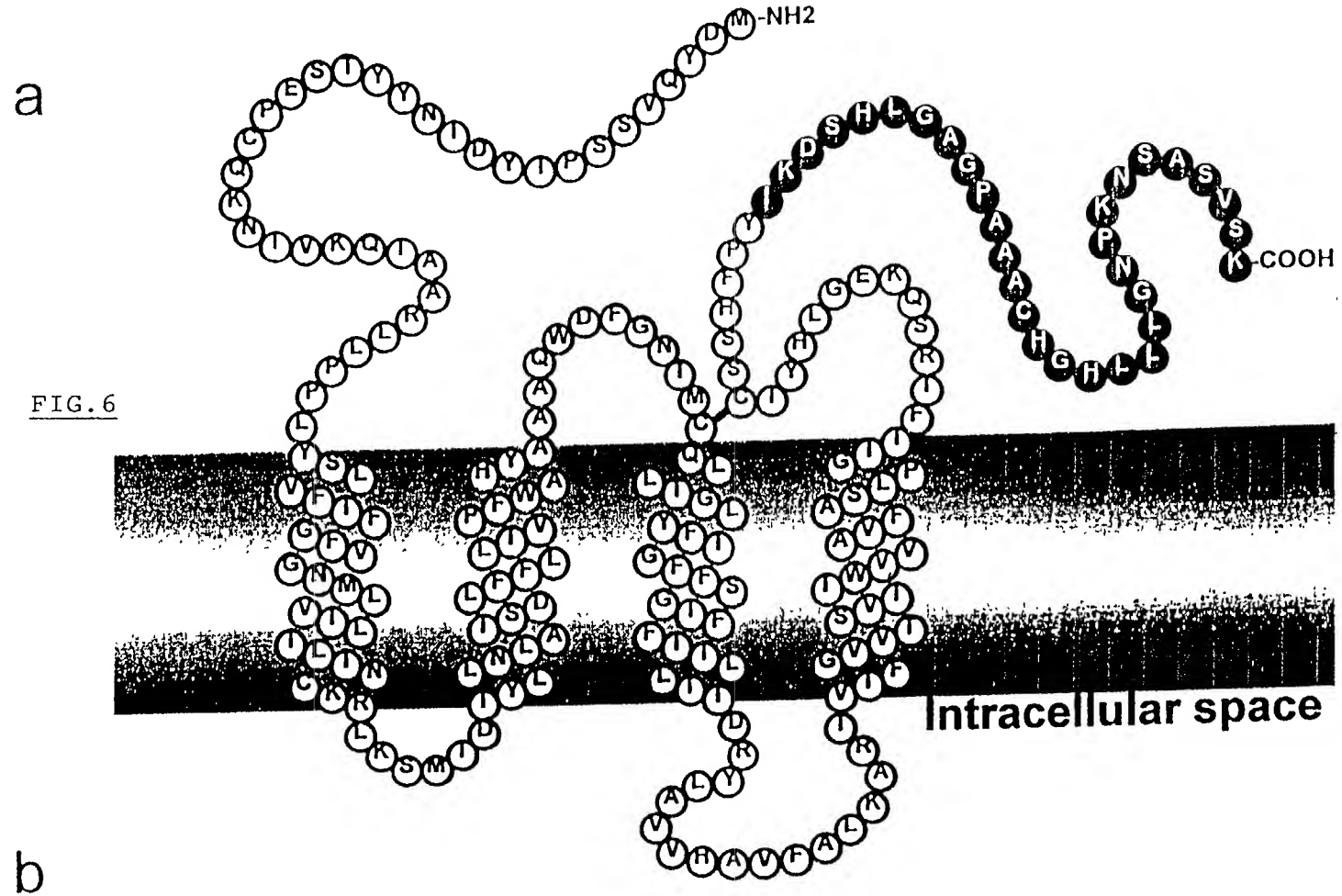

CCR5
HL-60
THP-1
MEG-01
KG-1A
JURKAT
RAJI
HEL 92.1.7
K-562
PBMC
CHO-WT
28 S
18 S

FIG.5

FIG.6


a
-NH2
-COOH
Intracellular space
b
CCR5 F P Y S Q Y Q F W K N F Q T L K I V I L G L V L P
TTTCCATACAgtcagtatcaattctggaagaatttccagacaTTAAAGATAGTCATCTTGGGGCTGGTCCTGCCG
Δccr5 F P Y
deletion
I K D S H L G A G P A
CCR5 L L V M V I C Y S G I L K T L L R C R N E K K R
CTGCTTGTCATGGTCATCTGCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGG
Δccr5 A A C H G H L L L G N P K N S A S V S K *

A.

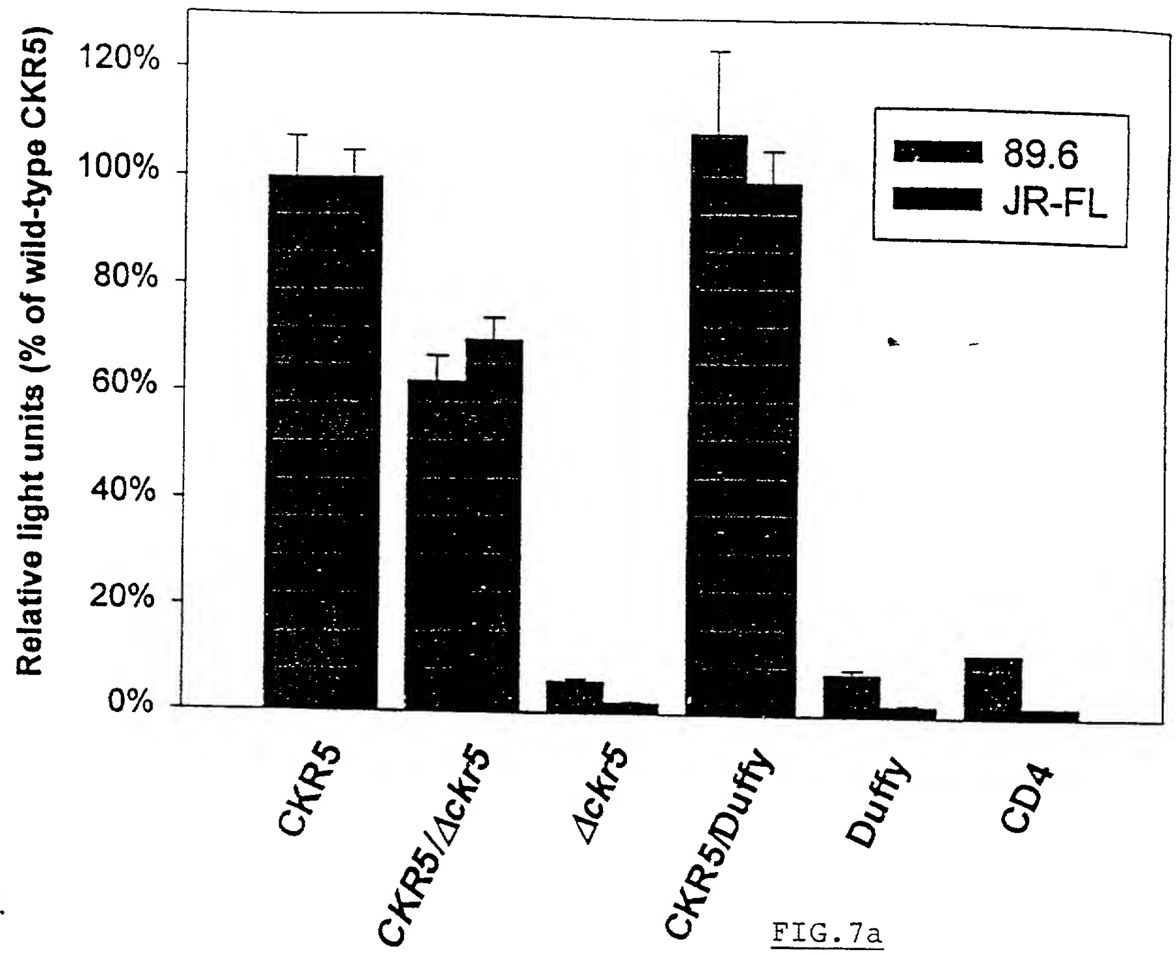


FIG.7a

B.

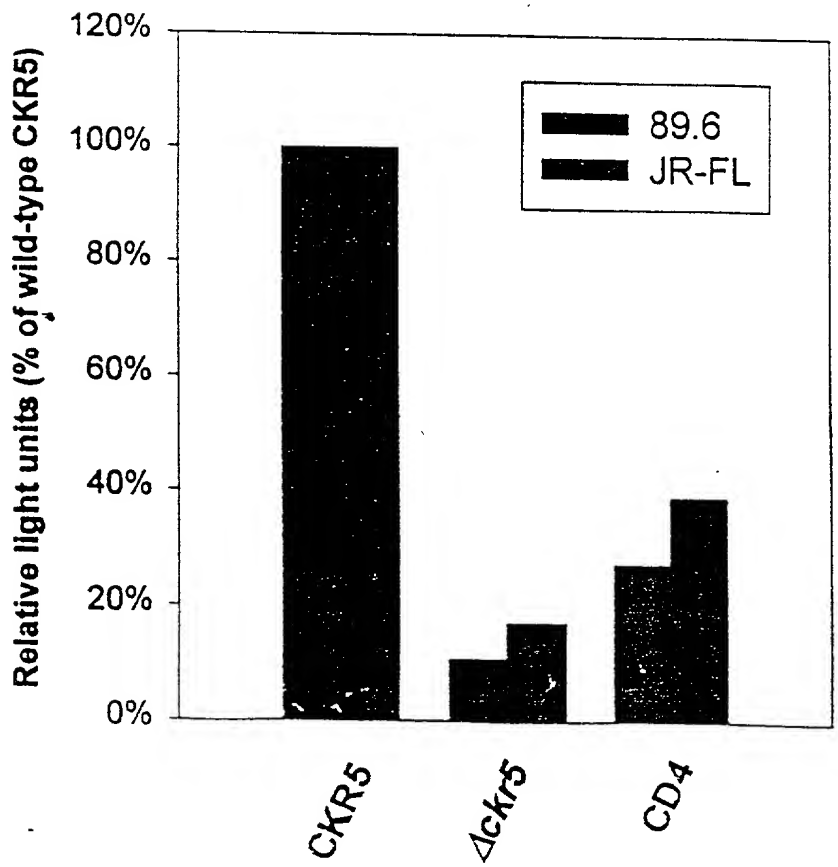


FIG.7b

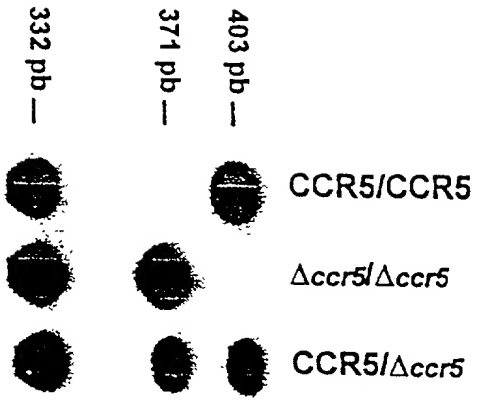


FIG.8

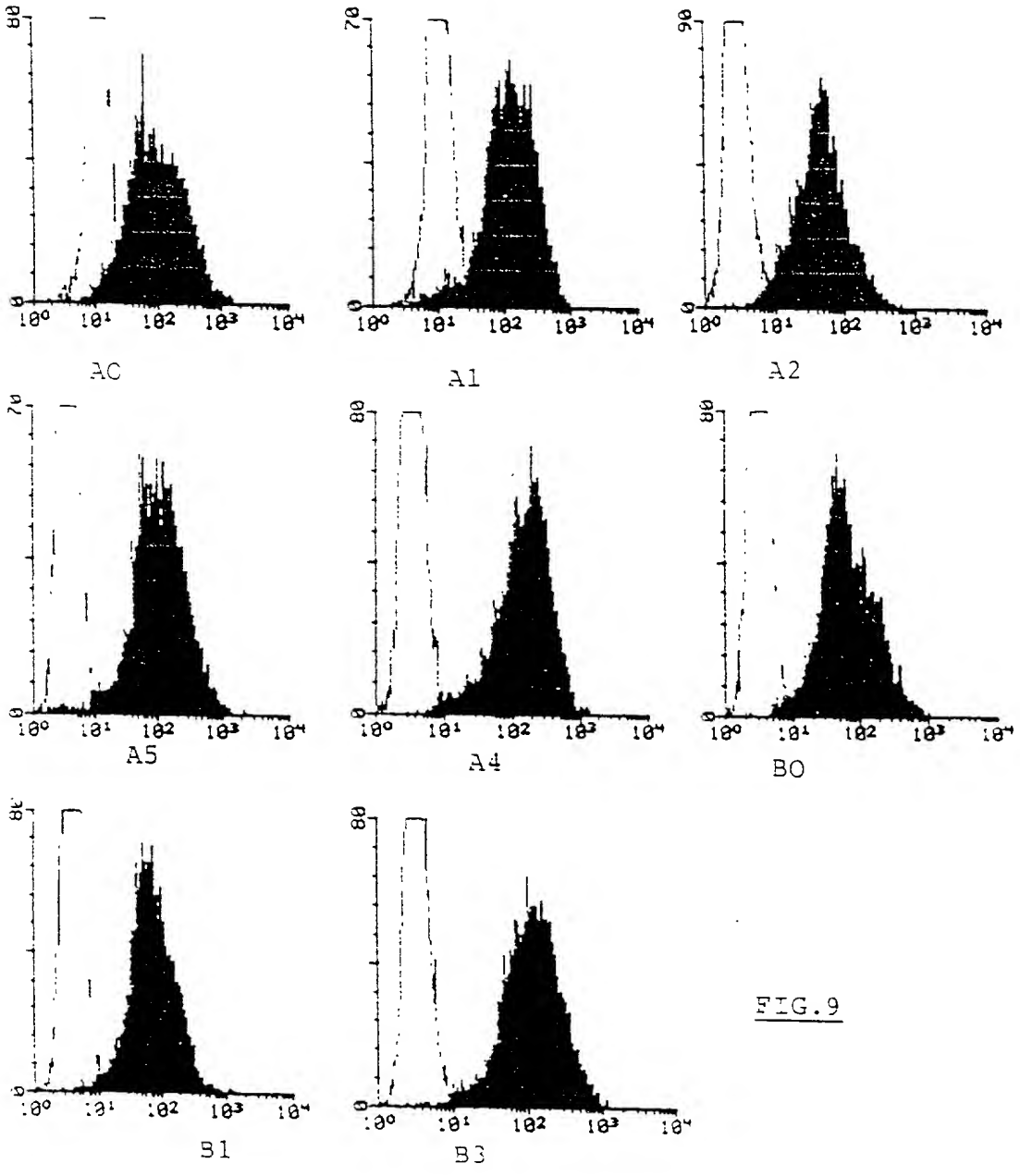


FIG.9

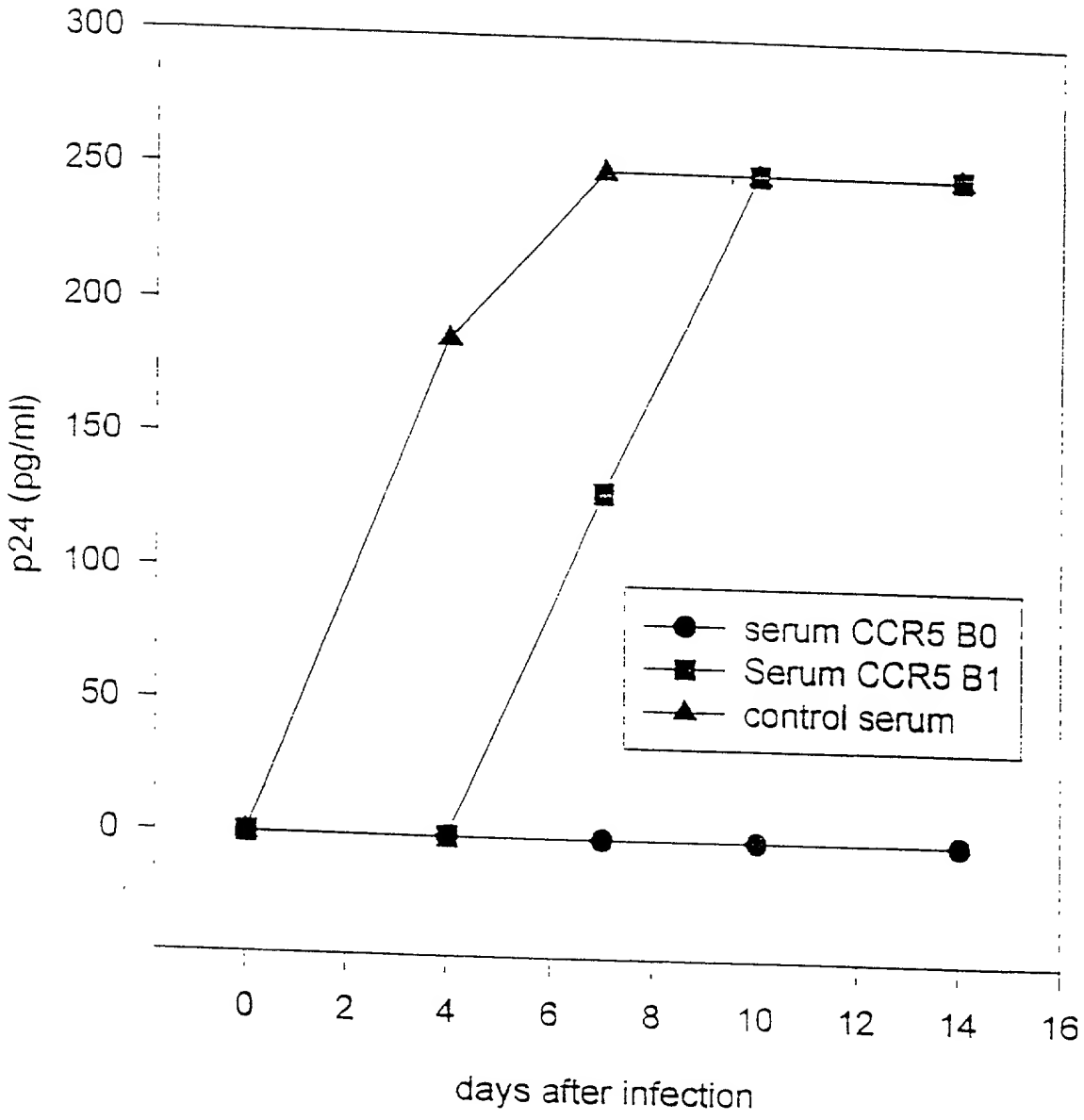

300
250
200
150
100
50
0
p24 (pg/ml)
0
2
4
6
8
10
12
14
16
days after infection
serum CCR5 B0
Serum CCR5 B1
control serum

FIG.10